

Inventors: Goodlett and Keller  
Serial No.: 09/835,072  
Filed: April 13, 2001  
Page 2

Please replace the paragraph starting on page 55, line 9, and ending on page 55, line 23, with the following paragraph:

--An additional optional feature in the method is the inclusion of internal multiple amino acid edges to account for degenerate sequence. These edges can enable a direct jump over a missing ion edge and assign that edge a degenerate amino acid designation. For example, a *de novo* derived sequence, - PDNAVITIG- (SEQ ID NO: 8), from a carboxyl-terminus labeled peptide can differ from the true sequence, SYELPDGQVITIGNER (SEQ ID NO: 7), at a di-amino acid stretch (i.e. NA vs. GQ) due to preferential cleavage at the leucinyI-proline bond that results in a missing y-9 fragment ion. A method with internal multiple amino acid edges can jump from the y-8 to the y-10 ion and the resulting sequence will have a degenerate amino acid at the y-9 position so that the resulting sequence will include the correct sequence.--

Please replace the paragraph starting on page 66, line 6, and ending on page 66, line 17, with the following paragraph:

Inventors: Goodlett and Keller  
Serial No.: 09/835,072  
Filed: April 13, 2001  
Page 3

--Table 1: Relative Abundance and Sequence of Select [M + 2H]<sup>2+</sup>  
ions

<u>d0-/d3-ester</u>	<u>Parent Protein</u>	<u>Database Sequence</u>	<u>NO:</u>	<u>de novo sequence</u>	<u>NO:</u>
1.0:1.0	VIME_HUMAN	QDVNASLAR	1	QDVNAS-	2
		QQYESVAAK	3	QQYESVAAK	3
1.0:1.1	ACTA_HUMAN	QEYDESGPSIVHR	4	QEYDESGP-	5
		AGFAGDDAPR	6	AGFAGDDAPR	6
		SYELPDGQVITIGNER	7	-PDNAVITIG-	8
1.0:1.2	GB01_HUMAN	LLLLGAGESGK	9	LLLLGAGE-	10
		GNLQIDFADPSR	11	-IDFAD-	12
1.0:1.7*	MYSN_HUMAN	DLEAHIDSANK	13	DLEAHID-	14

\*Not an average.

NO: indicates sequence identification number (SEQ ID NO:)--

Please replace the paragraph starting on page 17,  
line 27, and ending on page 18, line 2, with the following  
paragraph:

--As used herein, the term "low resolution" when  
referring to a mass spectrum is intended to mean that the mass  
determination is accurate at about twenty-five parts per million  
(ppm) or greater of component ion fragments. A mass spectrometer  
that provides an accuracy of less than about 25 ppm is considered  
to provide high resolution spectra.--

#### REMARKS

Claims 1-55 are currently pending in the application,  
and claims 1-4, 6, 8-13, 15-19, 21, and 23-29 are currently under  
examination.